

JAMS_version	JAMS v1.24
JAMS_Kdb_Version	JAMSk2all32_1.21_1553224440
Sample_name	SRR3656745sub120M
Run_start	2019-04-17 18:50:40
Run_end	2019-04-18 06:47:19
Duration_hours	11.94
CPUs_used	48
Run_type	metagenome
Process	Assemble_from_reads
Sequencing_chemistry	illuminape
Library_strategy	pairedend
Contig_assembler	megahit
Contig_assembler_version	MEGAHIT v1.1.3
Host_species	none

Just A Microbiology System

JAMS version 1.27

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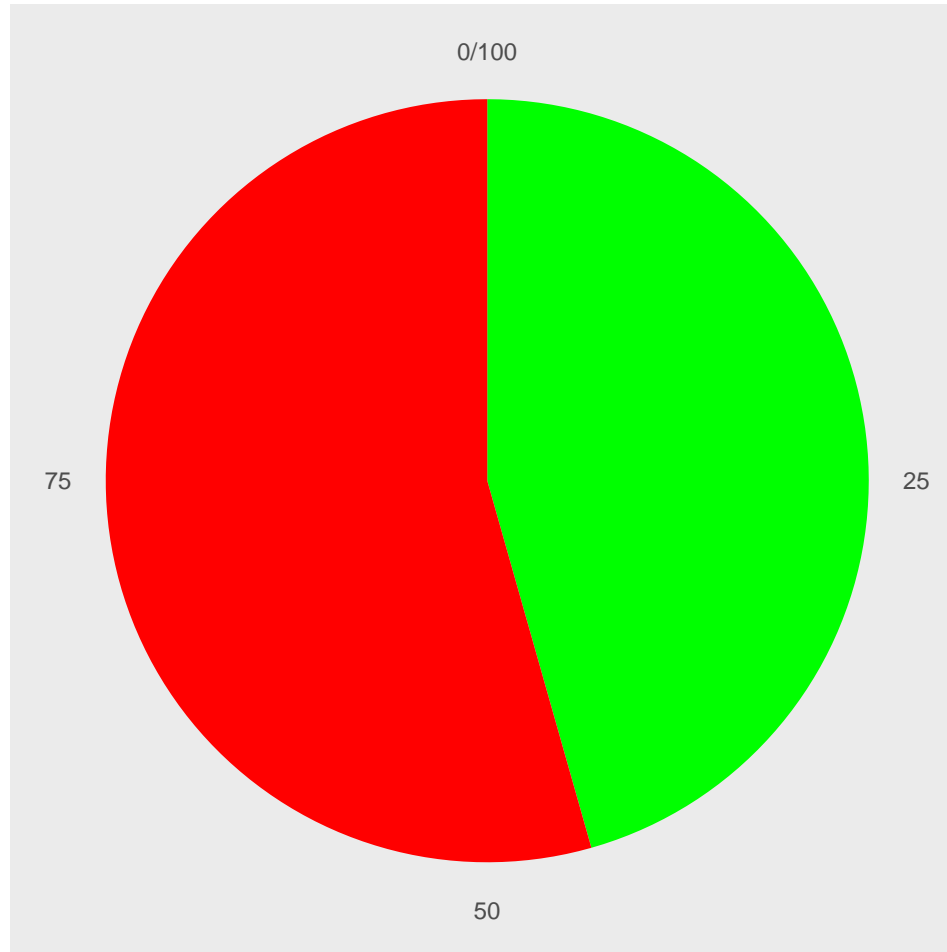
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National Cancer Institute

National Institutes of Health

Bethesda, MD, USA

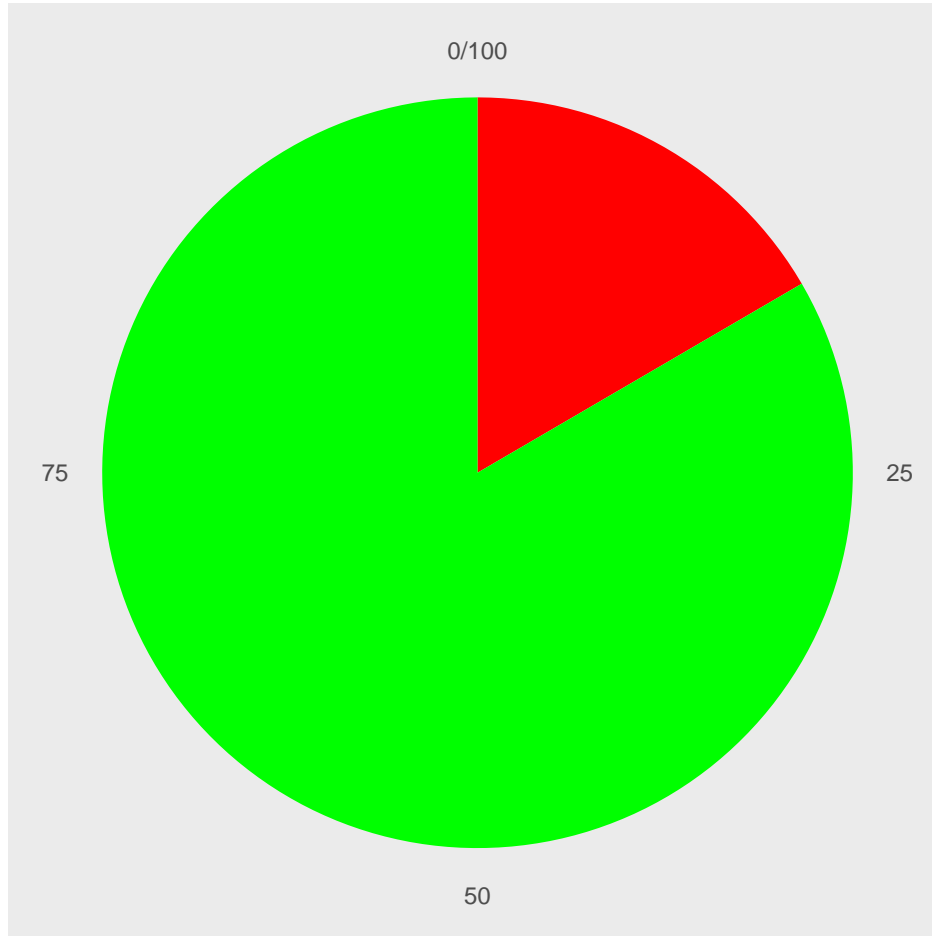
SRR3656745sub120M – % Bases Passing QC



survivingQC

- Not-surviving=54.4%
- Surviving=45.6%

SRR3656745sub120M – % Bases Assembled into Contigs

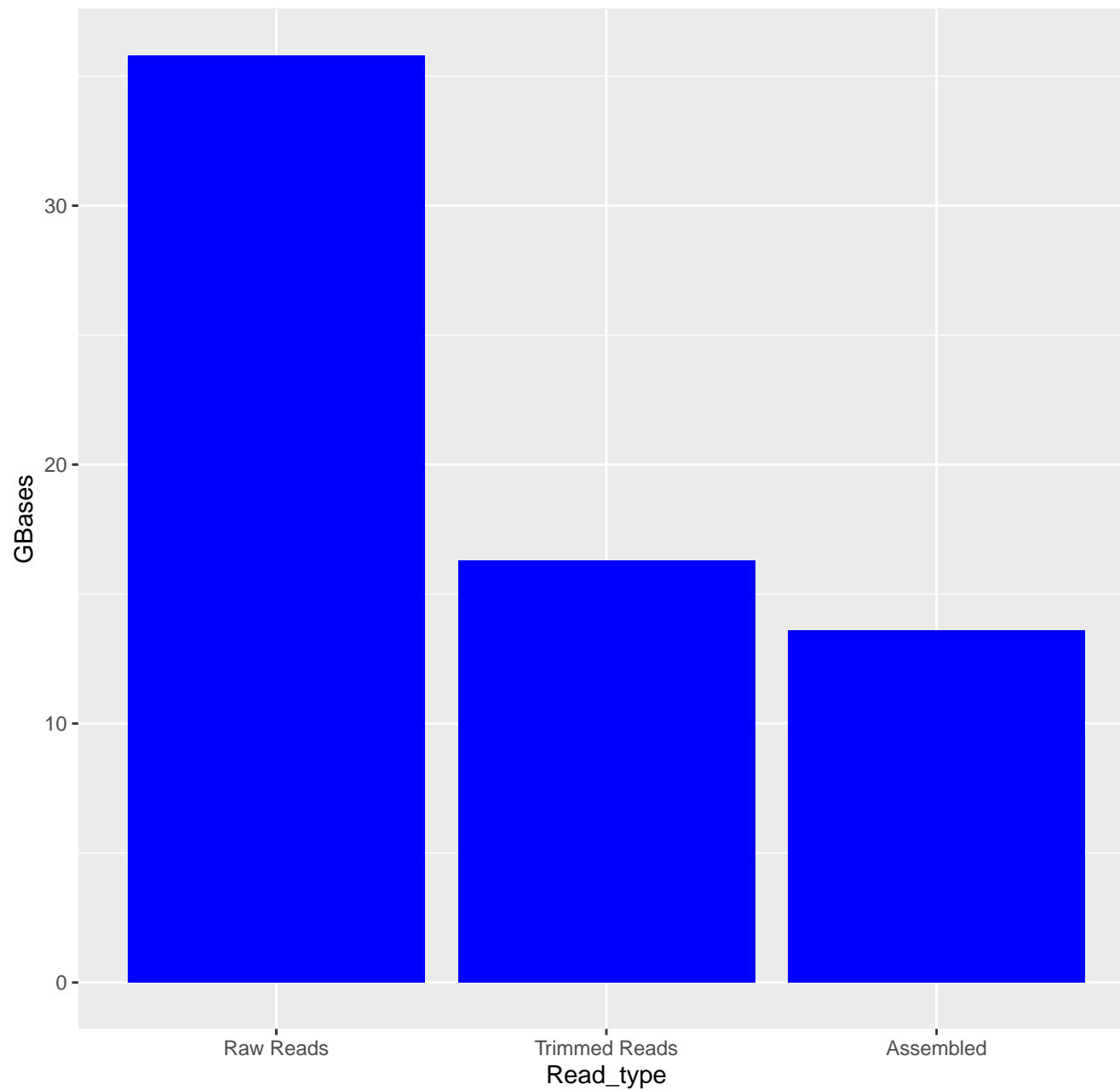


Assembled_bases

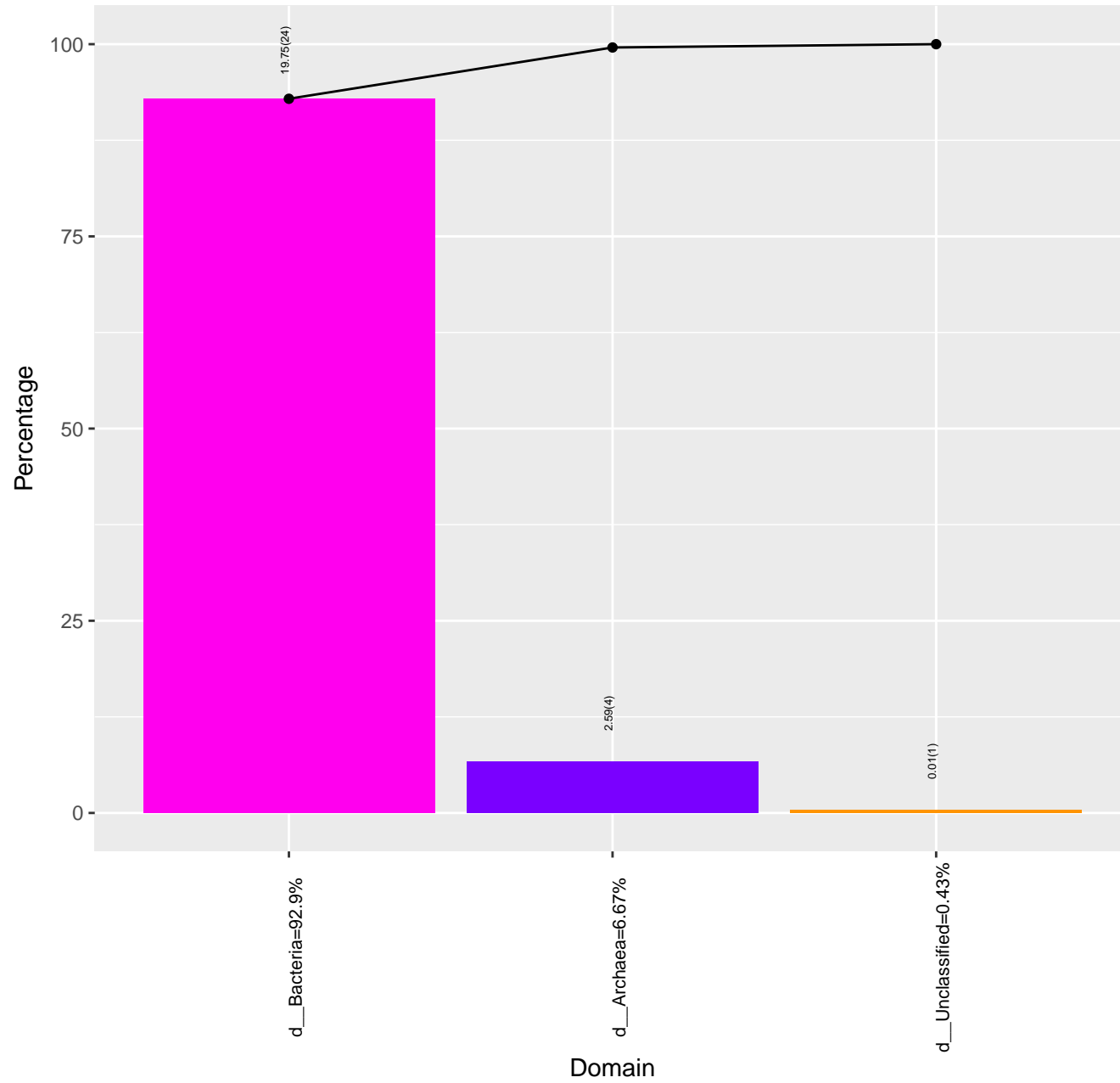
Assembled=83.4%

Not Assembled=16.6%

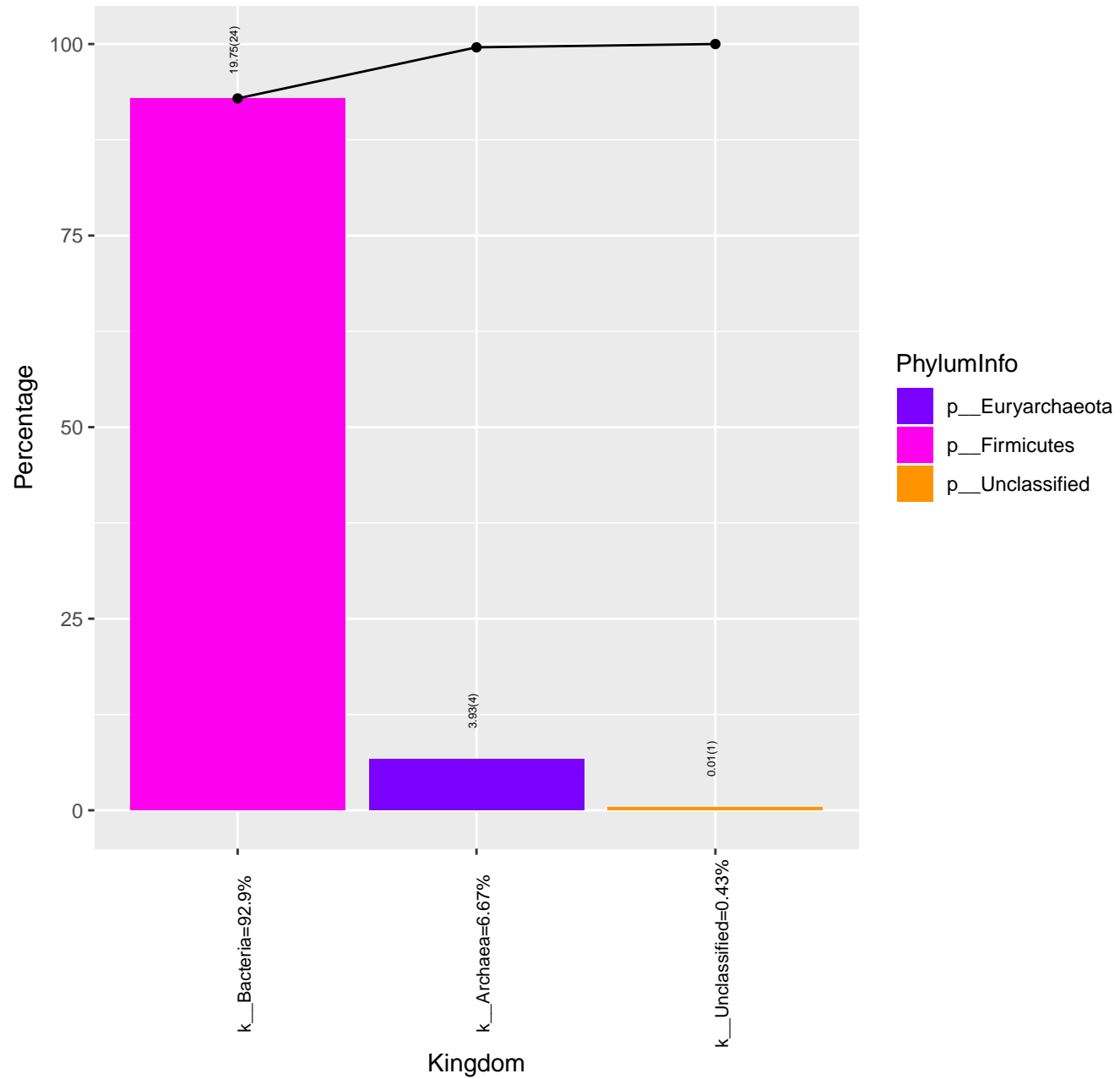
SRR3656745sub120M – Total Basepairs per Read Type (Gbp)



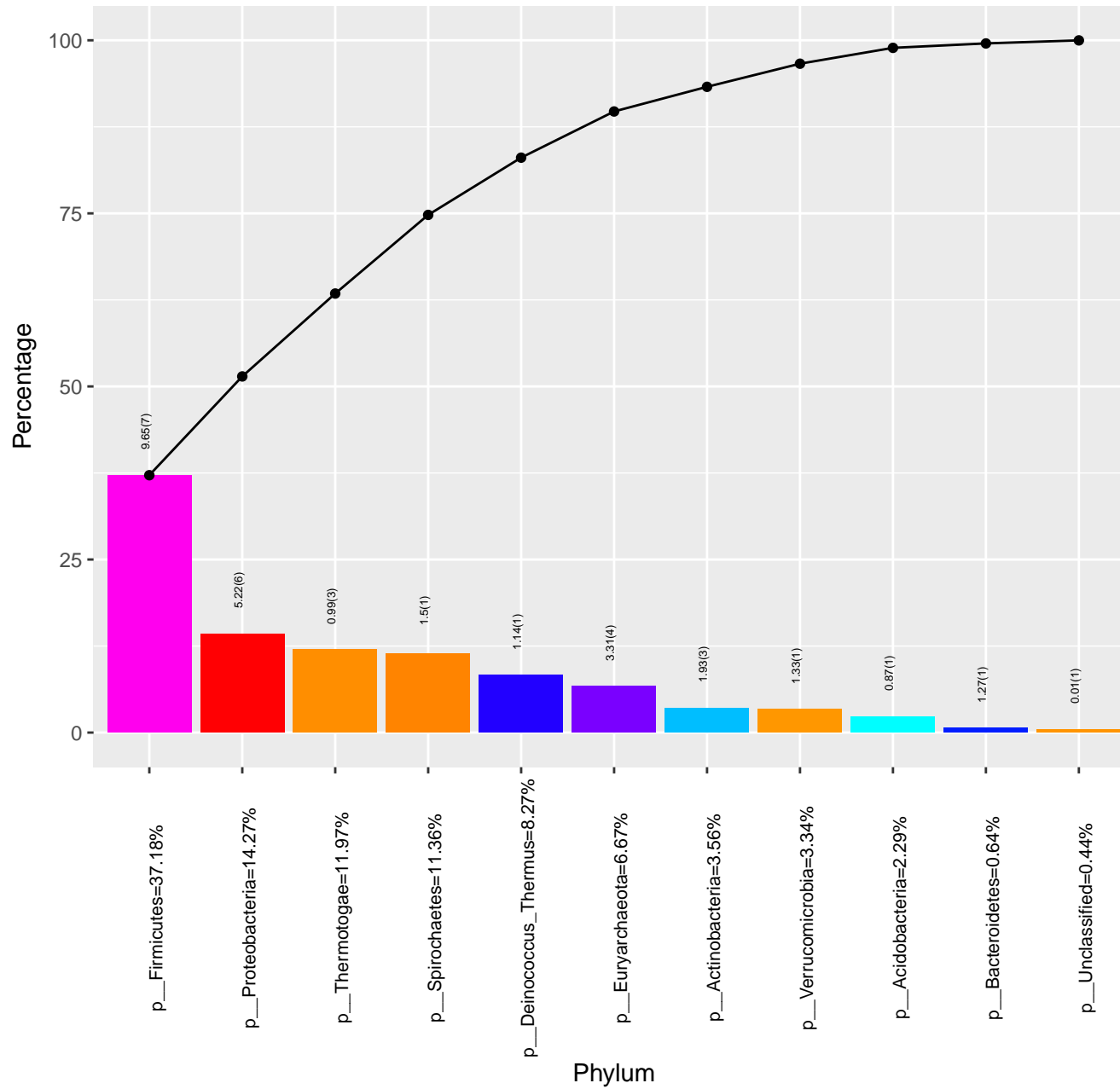
Taxonomic relative abundance – Domain in SRR3656745sub120M



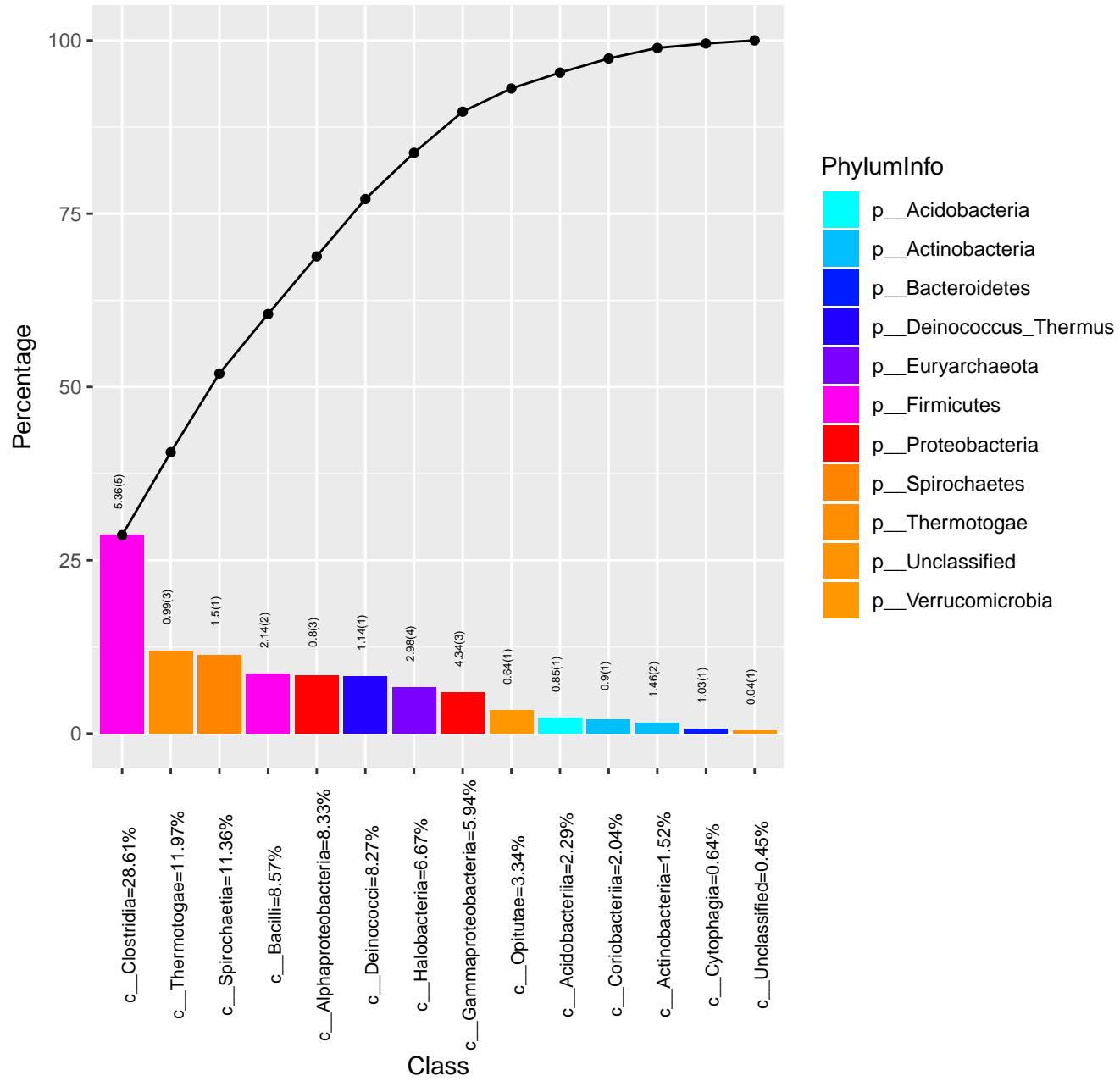
Taxonomic relative abundance – Kingdom in SRR3656745sub120M



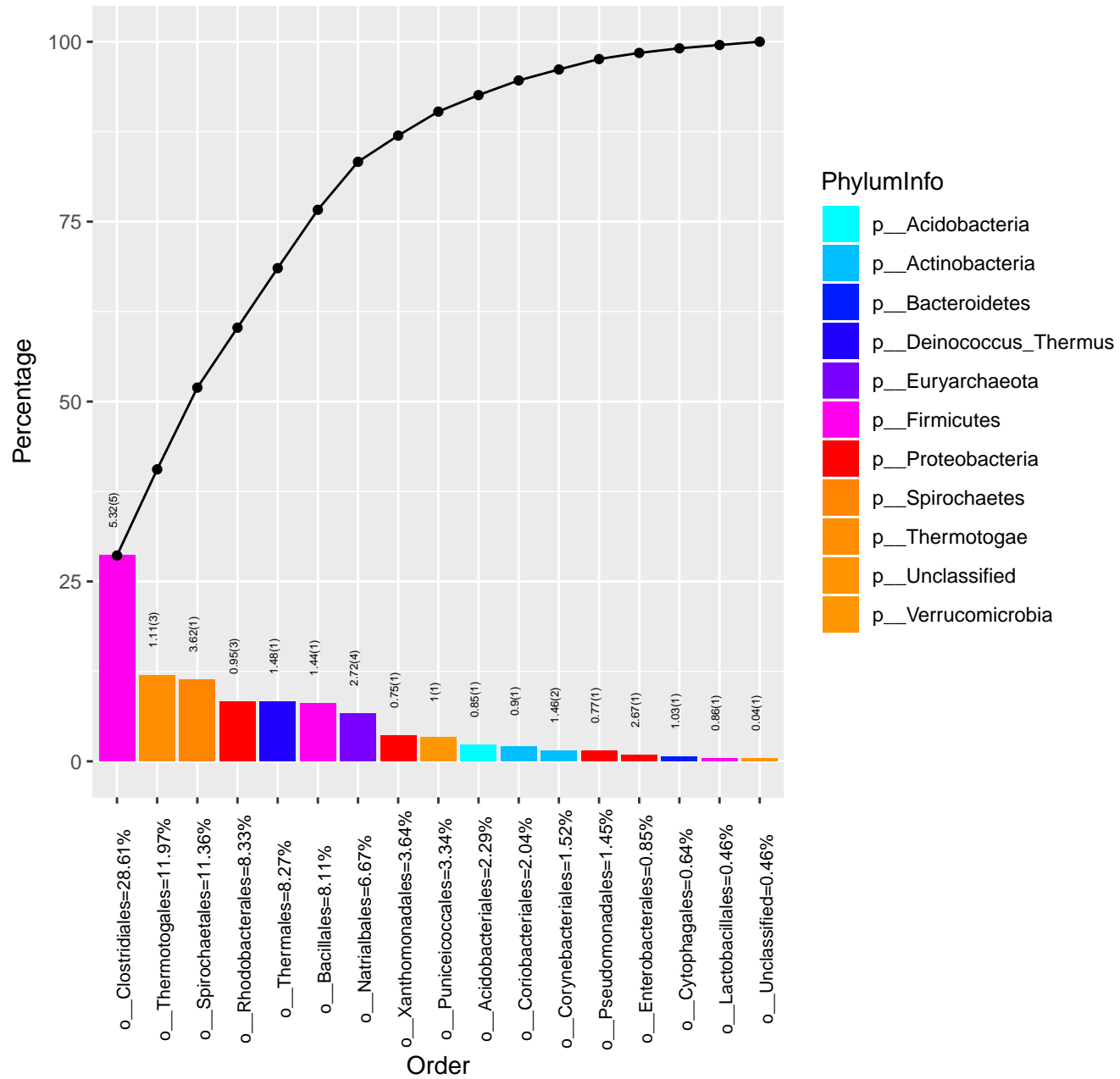
Taxonomic relative abundance – Phylum in SRR3656745sub120M



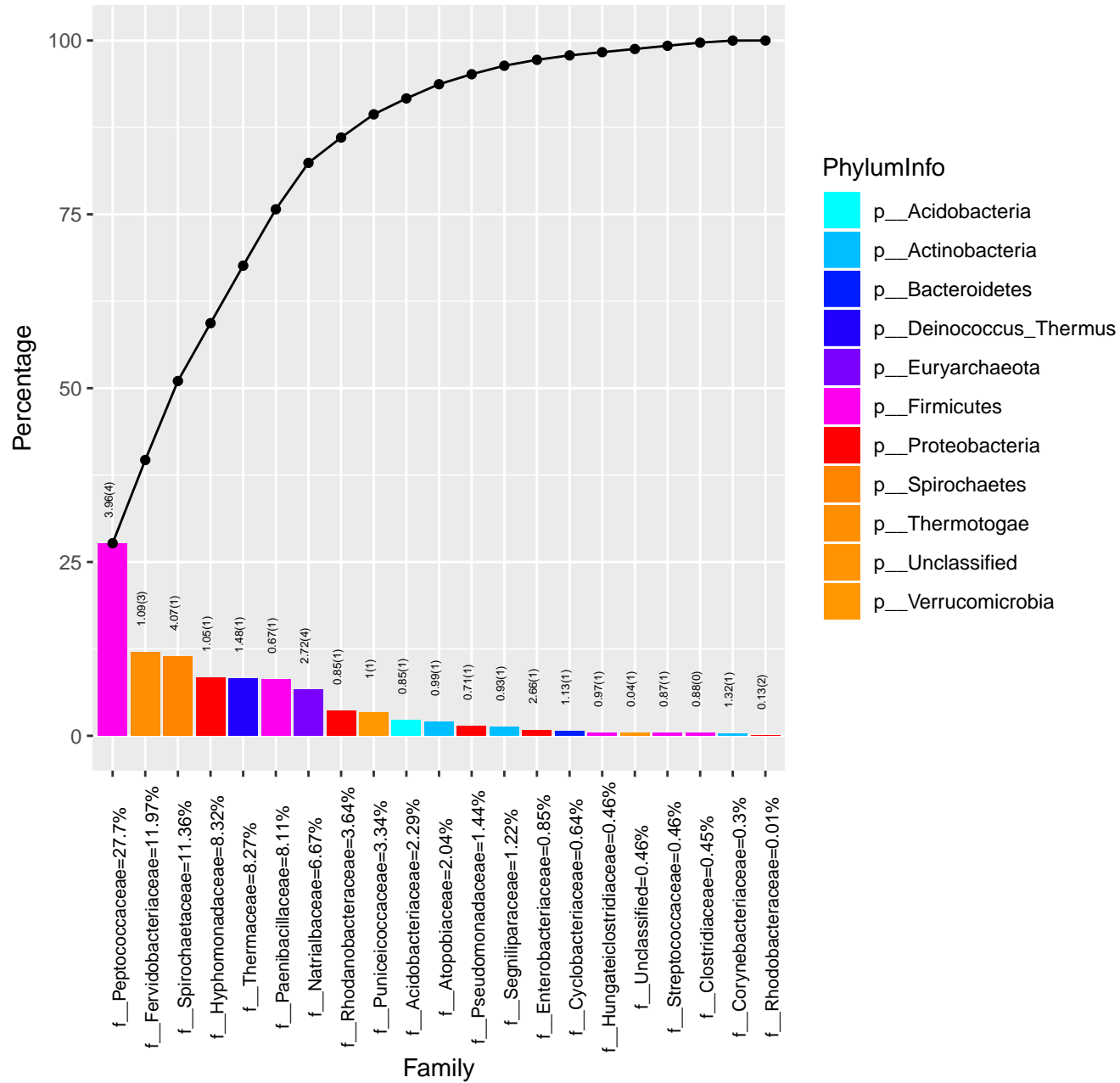
Taxonomic relative abundance – Class in SRR3656745sub120M



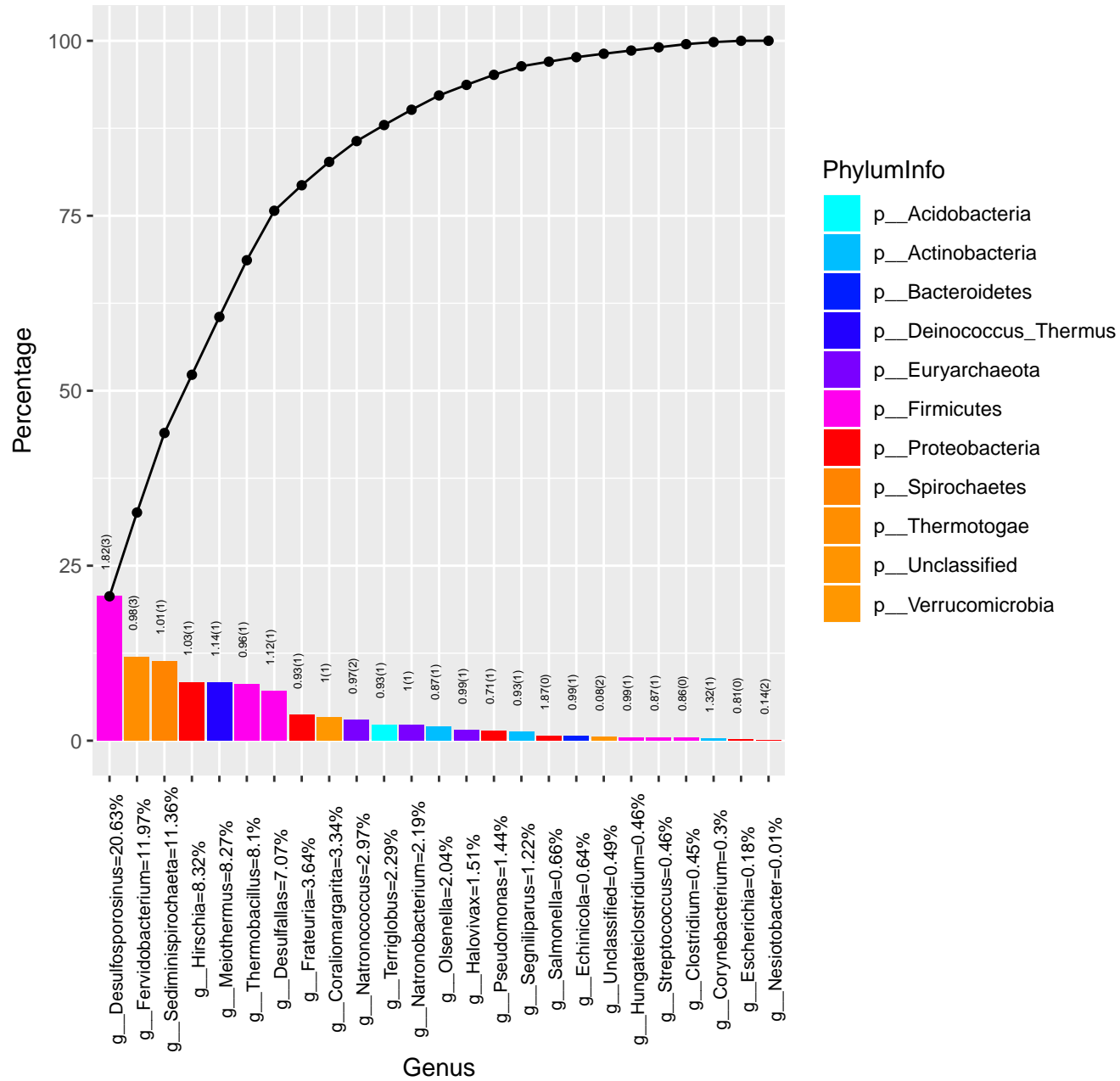
Taxonomic relative abundance – Order in SRR3656745sub120M



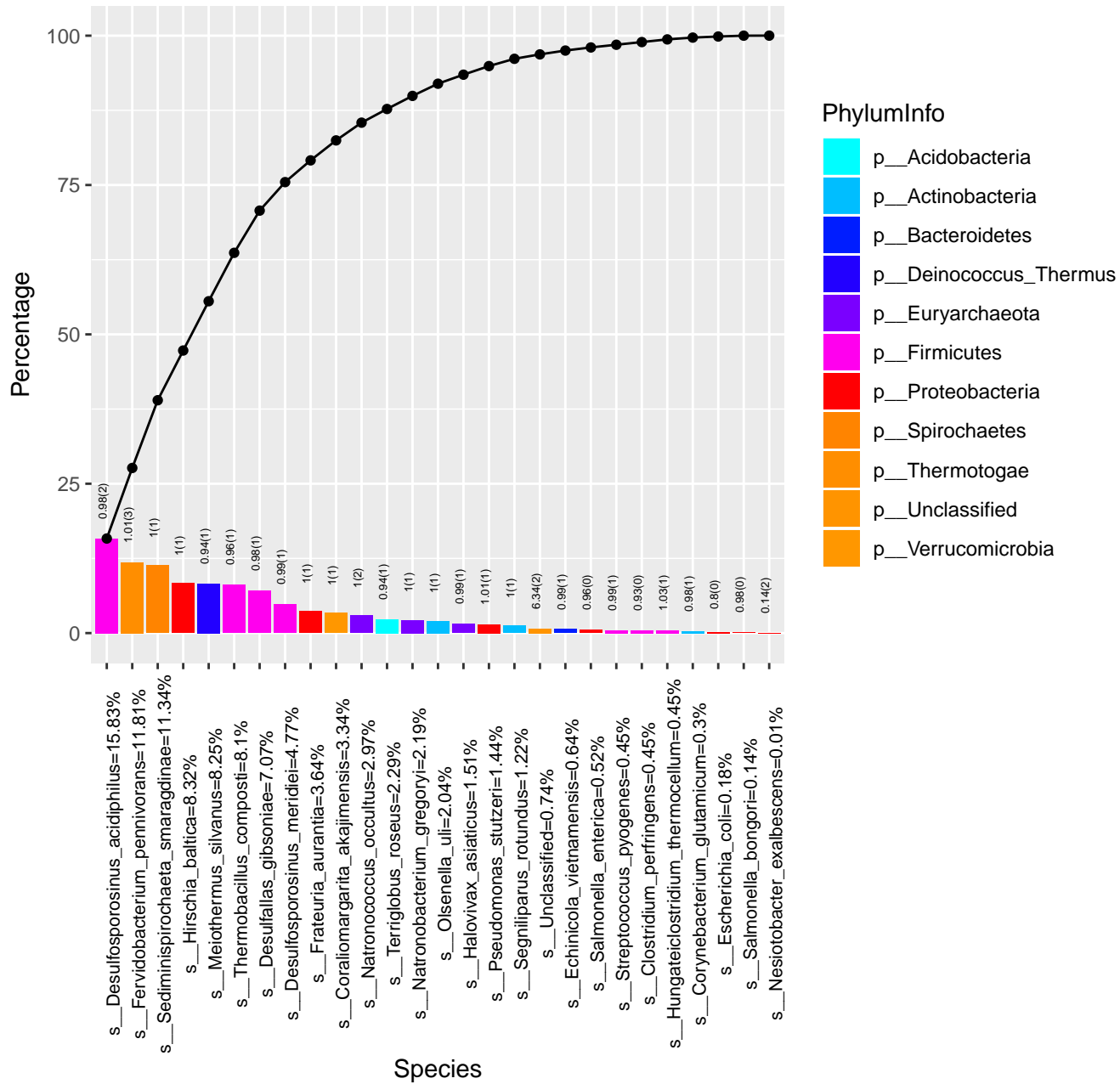
Taxonomic relative abundance – Family in SRR3656745sub120M



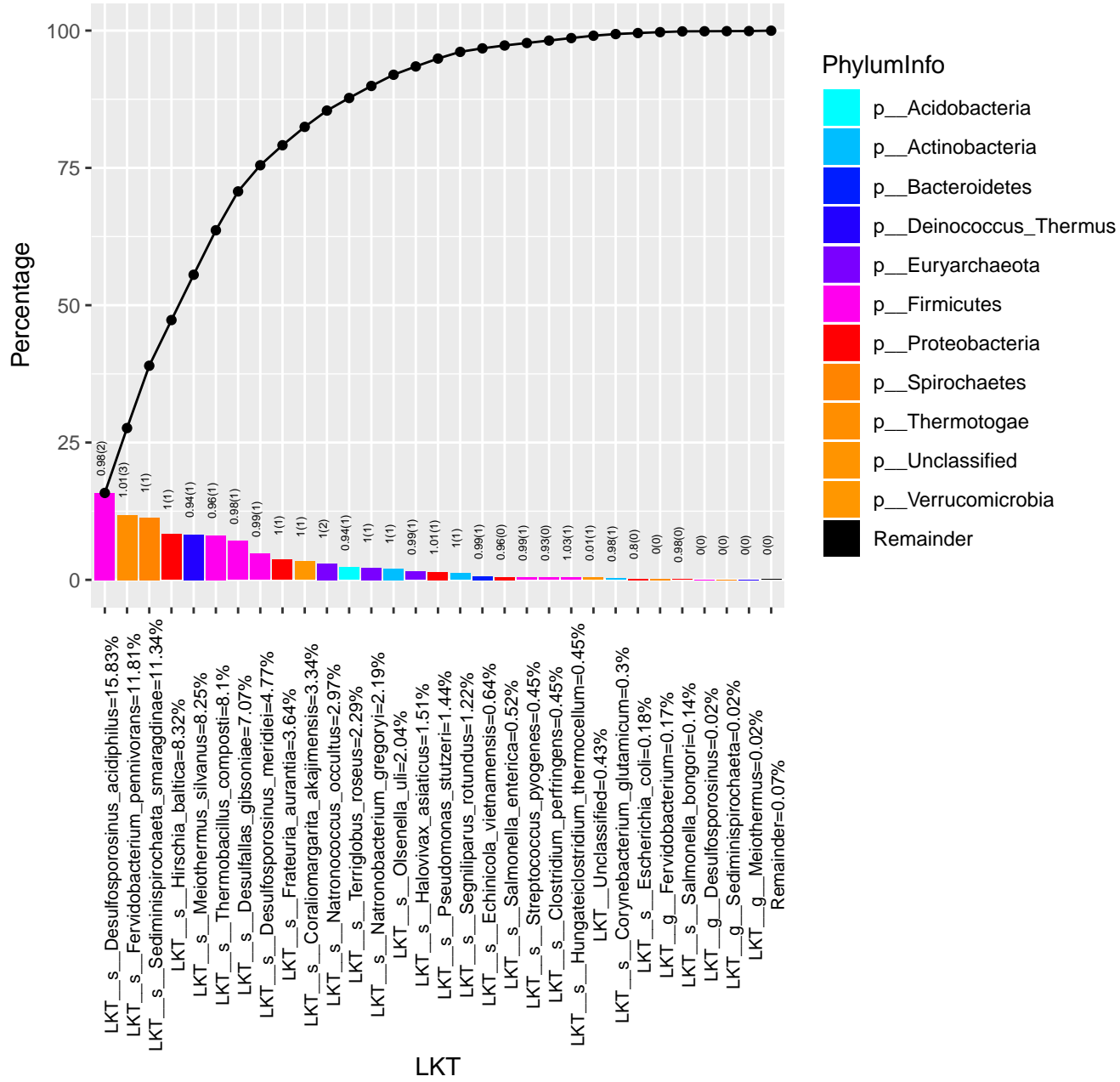
Taxonomic relative abundance – Genus in SRR3656745sub120M



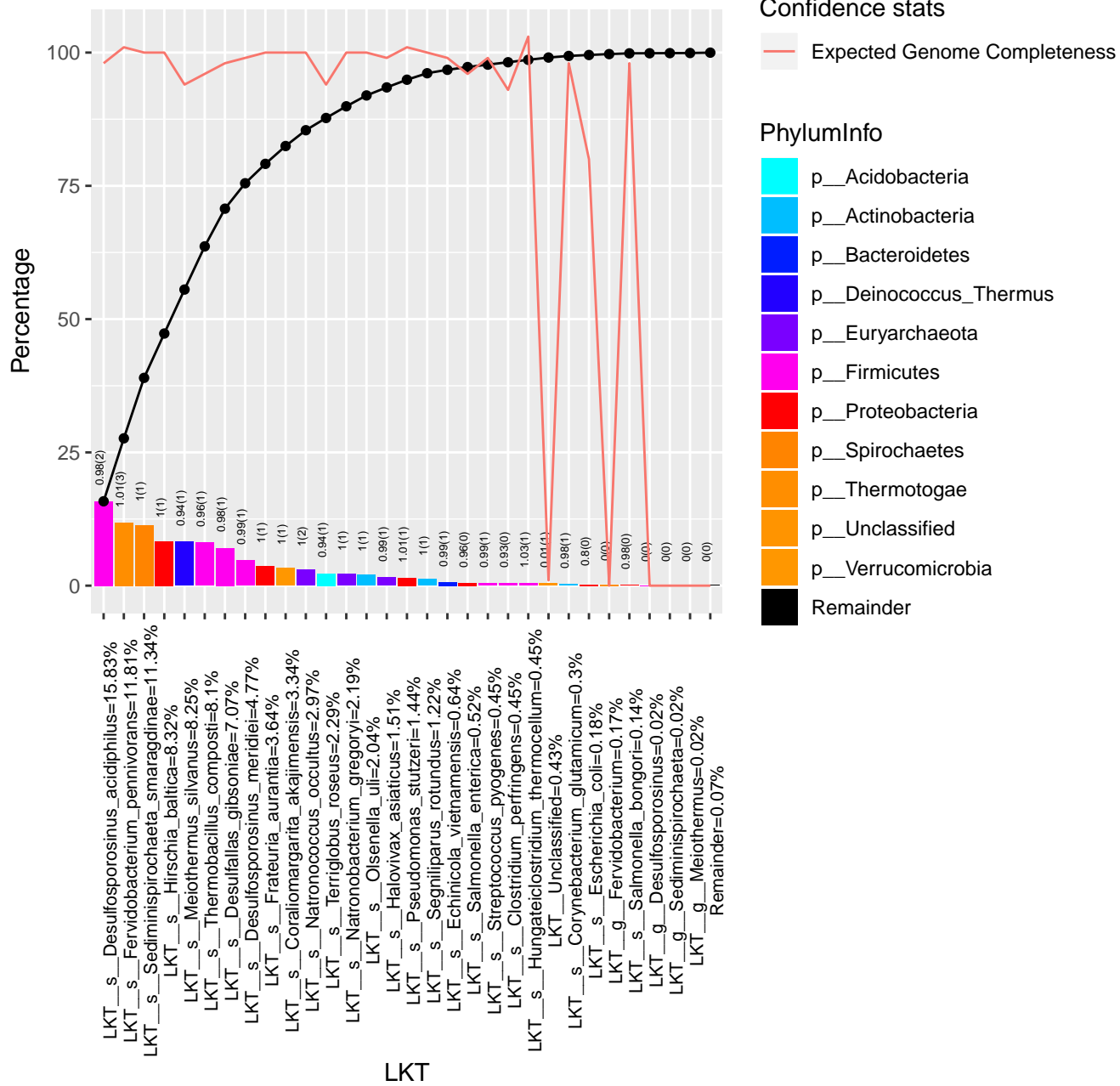
Taxonomic relative abundance – Species in SRR3656745sub120M



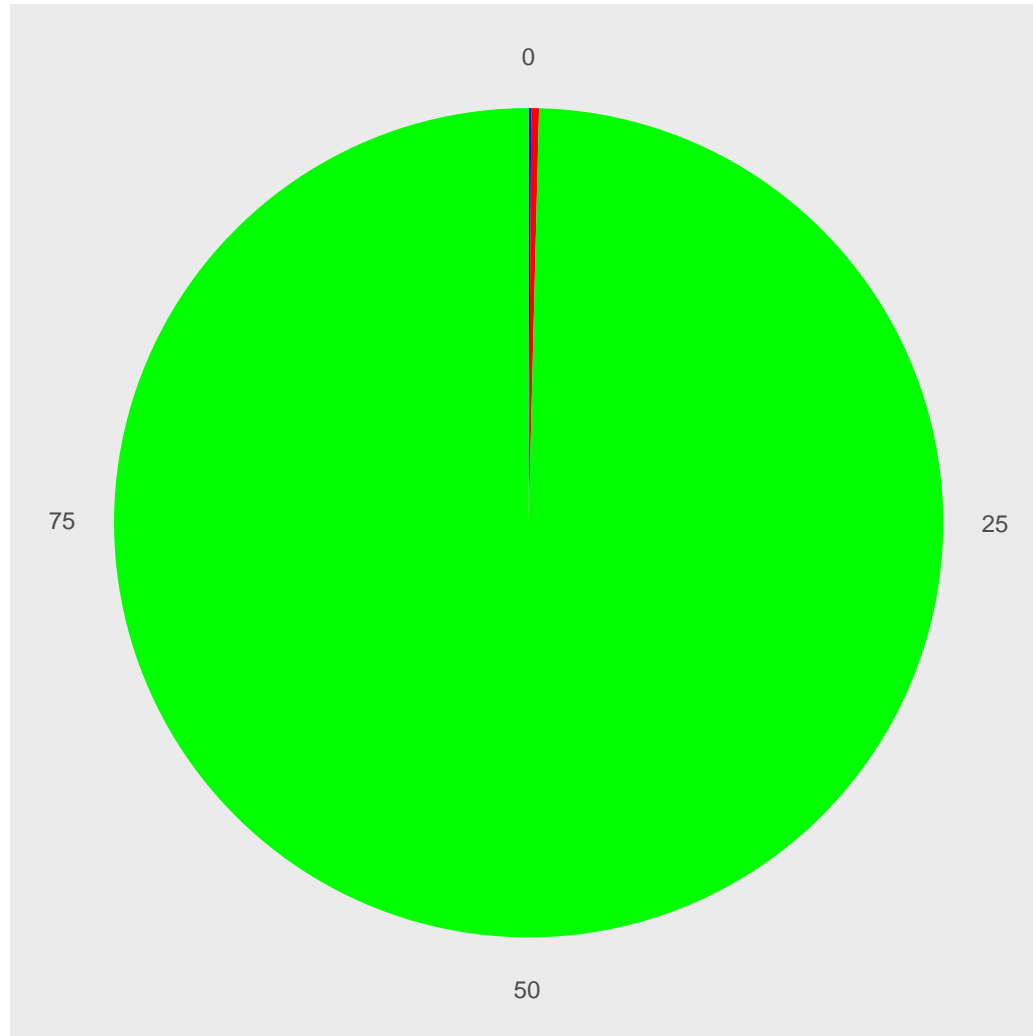
Taxonomic relative abundance – LKT in SRR3656745sub120M



Taxonomic relative abundance – LKT in SRR3656745sub120M



SRR3656745sub120M – % Feature type found in Contigs



Feature Type

- CDS = 99.5%
- rRNA = 0.3%
- tRNA = 0.1%

Consolidated 16S rRNA table

Gene	Length_16S	Contig	Contig_Length	LKT_dada2	LKT_kraken
SRR3656745sub120M_00066	1521	SRR3656745sub120M_ctg_0050	5571	LKT__Corynebacterium_glutamicum	LKT__s__Corynebacterium_glutamicum
SRR3656745sub120M_00149	1532	SRR3656745sub120M_ctg_0074	4373	LKT__Pseudomonas_Unclassified	LKT__s__Pseudomonas_stutzeri
SRR3656745sub120M_00244	441	SRR3656745sub120M_ctg_0109	2979	LKT__Natronococcus_Unclassified	LKT__s__Natronococcus_occultus
SRR3656745sub120M_07079	716	SRR3656745sub120M_ctg_0691	720	LKT__Desulfosporosinus_meridiei	LKT__s__Desulfosporosinus_meridiei
SRR3656745sub120M_07994	709	SRR3656745sub120M_ctg_0749	711	LKT__Fervidobacterium_Unclassified	LKT__s__Fervidobacterium_pennivorans
SRR3656745sub120M_10701	1541	SRR3656745sub120M_ctg_0846	4552	LKT__Frateuria_Unclassified	LKT__s__Frateuria_aurantia
SRR3656745sub120M_10936	1466	SRR3656745sub120M_ctg_0859	4445	LKT__Halovivax_Unclassified	LKT__s__Halovivax_asiaticus
SRR3656745sub120M_11540	1294	SRR3656745sub120M_ctg_0906	1306	LKT__Clostridium_perfringens	LKT__Unclassified
SRR3656745sub120M_12013	1476	SRR3656745sub120M_ctg_0921	1507	LKT__Thermobacillus_Unclassified	LKT__s__Thermobacillus_composti
SRR3656745sub120M_13260	1545	SRR3656745sub120M_ctg_0962	5196	LKT__Streptococcus_pyogenes	LKT__s__Streptococcus_pyogenes
SRR3656745sub120M_13690	442	SRR3656745sub120M_ctg_0968	3048	LKT__Natronobacterium_Unclassified	LKT__s__Natronobacterium_gregoryi
SRR3656745sub120M_13709	496	SRR3656745sub120M_ctg_0972	1178	LKT__Nesiotobacter_exalbescens	LKT__s__Nesiotobacter_exalbescens
SRR3656745sub120M_15149	966	SRR3656745sub120M_ctg_1049	967	LKT__Natronococcus_Unclassified	LKT__s__Natronococcus_occultus
SRR3656745sub120M_19545	1539	SRR3656745sub120M_ctg_1254	1677	LKT__Sediminispirochaeta_Unclassified	LKT__s__Sediminispirochaeta_smaragdinae
SRR3656745sub120M_24058	460	SRR3656745sub120M_ctg_1475	534	LKT__Desulfosporosinus_Unclassified	LKT__s__Desulfosporosinus_acidiphilus
SRR3656745sub120M_30474	699	SRR3656745sub120M_ctg_1850	703	LKT__Desulfotomaculum_gibsoniae	LKT__s__Desulfallas_gibsoniae
SRR3656745sub120M_38872	1498	SRR3656745sub120M_ctg_2119	6420	LKT__Terriglobus_Unclassified	LKT__s__Terriglobus_roseus
SRR3656745sub120M_39193	1526	SRR3656745sub120M_ctg_2147	1732	LKT__Ruminiclostridium_Unclassified	LKT__s__Hungateiclostridium_thermocellum
SRR3656745sub120M_40112	1513	SRR3656745sub120M_ctg_2194	106345	LKT__Segniliparus_Unclassified	LKT__s__Segniliparus_rotundus
SRR3656745sub120M_43589	1519	SRR3656745sub120M_ctg_2351	1559	LKT__Echinicola_Unclassified	LKT__s__Echinicola_vietnamensis

Consolidated 16S rRNA table

Gene	Length_16S	Contig	Contig_Length	LKT_dada2	LKT_kraken
SRR3656745sub120M_50349	950	SRR3656745sub120M_ctg_2665	984	LKT__Desulfosporosinus_acidiphilus	LKT__s__Desulfosporosinus_acidiphilus
SRR3656745sub120M_58841	1291	SRR3656745sub120M_ctg_2994	1295	LKT__f__Enterobacteriaceae	LKT__f__Enterobacteriaceae
SRR3656745sub120M_61032	454	SRR3656745sub120M_ctg_3090	1194	LKT__Nesiotobacter_exalbescens	LKT__s__Nesiotobacter_exalbescens
SRR3656745sub120M_61857	1446	SRR3656745sub120M_ctg_3138	5938	LKT__Hirschia_Unclassified	LKT__s__Hirschia_baltica
SRR3656745sub120M_62811	582	SRR3656745sub120M_ctg_3163	8416	LKT__Fervidobacterium_Unclassified	LKT__s__Fervidobacterium_pennivorans
SRR3656745sub120M_65756	582	SRR3656745sub120M_ctg_3265	17141	LKT__Fervidobacterium_Unclassified	LKT__s__Fervidobacterium_pennivorans
SRR3656745sub120M_73036	1490	SRR3656745sub120M_ctg_3626	1503	LKT__Meiothermus_Unclassified	LKT__s__Meiothermus_silvanus
SRR3656745sub120M_78072	1551	SRR3656745sub120M_ctg_3797	5838	LKT__Coraliomargarita_Unclassified	LKT__s__Coraliomargarita_akajimensis
SRR3656745sub120M_80334	1511	SRR3656745sub120M_ctg_3824	319903	LKT__Olsenella_Unclassified	LKT__s__Olsenella_uii

Known antibiotic resistance genes

DB_Hit	Function	Percent_ID	Contig	Length	LKT
mdf(A)_1_Y08743	Macrolide, Aminoglycoside, Tetracycline, Fluoroquinolone, Phenicol, Rifampicin	99.919	SRR3656745sub120M_ctg_1770	54903	LKT__s__Escherichia_coli
cmr_1_U43535	Macrolide, Tetracycline	100	SRR3656745sub120M_ctg_3000	231358	LKT__s__Corynebacterium_glutamicum
msr(D)_3_AF227520	Macrolide, Streptogramin B	77.716	SRR3656745sub120M_ctg_3352	47135	LKT__s__Desulfosporosinus_meridiei

Virulence factors present in VFDB
www.ncbi.nlm.nih.gov/pubmed/15608208

DB_Hit	Function	Percent_ID	LKT
vfdb---csgF---NP_460111	Curli_production_assembly_transport_component_CsgF	89.855	LKT__s__Escherichia_coli
vfdb---csgE---NP_460112	Curli_production_assembly_transport_component_CsgE	90.076	LKT__s__Escherichia_coli
vfdb---csgD---NP_460113	CsgBAC_operon_transcriptional_regulatory_protein	92.13	LKT__s__Escherichia_coli
vfdb---csgB---NP_460114	Minor_curlin_subunit	82.119	LKT__s__Escherichia_coli
vfdb---fliA---YP_001006726	RNA_polymerase_sigma_factor_FliA	82.353	LKT__s__Salmonella_enterica
vfdb---rfaD---NP_439271	ADP-L-glycero-D-manno-heptose-6-epimerase	77.597	LKT__s__Salmonella_enterica
vfdb---espY1---NP_285753	hypothetical_protein	87.5	LKT__s__Escherichia_coli
vfdb---fliA---YP_001006726	RNA_polymerase_sigma_factor_FliA	82.895	LKT__s__Salmonella_bongori
vfdb---fimD---NP_459541	Outer_membrane usher_protein_SfmD	96.207	LKT__s__Salmonella_enterica
vfdb---fimC---NP_459540	putative_fimbrial_chaperone_SfmC	92.609	LKT__s__Salmonella_enterica
vfdb---fimI---NP_459539	Type-1_fimbrial_protein_2C_A_chain	93.22	LKT__s__Salmonella_enterica
vfdb---ompA---AAF37887	Outer_membrane_protein_A	93.41	LKT__s__Salmonella_bongori
vfdb---fliM---YP_001006748	Flagellar_motor_switch_protein_FliM	84.685	LKT__s__Salmonella_bongori
vfdb---fliN---YP_001006749	Flagellar_motor_switch_protein_FliN	76.812	LKT__s__Salmonella_bongori
vfdb---fliP---YP_001006751	Flagellar_biosynthetic_protein_FliP	85.903	LKT__s__Salmonella_bongori
vfdb---csgG---NP_460110	Curli_production_assembly_transport_component_CsgG	98.917	LKT__s__Salmonella_bongori
vfdb---csgF---NP_460111	Curli_production_assembly_transport_component_CsgF	97.826	LKT__s__Salmonella_bongori
vfdb---csgE---NP_460112	Curli_production_assembly_transport_component_CsgE	93.13	LKT__s__Salmonella_bongori
vfdb---csgD---NP_460113	CsgBAC_operon_transcriptional_regulatory_protein	96.759	LKT__s__Salmonella_bongori
vfdb---csgB---NP_460114	Minor_curlin_subunit	98.013	LKT__s__Salmonella_bongori

Virulence factors present in VFDB
www.ncbi.nlm.nih.gov/pubmed/15608208

DB_Hit	Function	Percent_ID	LKT
vfdb---csgA---NP_460115	Major_curlin_subunit	100	LKT__s__Salmonella_bongori
vfdb---csgC---NP_460116	Curli_assembly_protein_CsgC	92.523	LKT__s__Salmonella_bongori
vfdb---sseK1---NP_463026	hypothetical_protein	97.024	LKT__s__Salmonella_enterica
vfdb---pfoA---NP_561079	Perfringolysin_O	99.8	LKT__s__Clostridium_perfringens
vfdb---colA---NP_561089	Microbial_collagenase	98.641	LKT__s__Clostridium_perfringens
vfdb---nagH---NP_561107	Hyaluronoglucosaminidase	98.403	LKT__s__Clostridium_perfringens
vfdb---csgC---NP_460116	Curli_assembly_protein_CsgC	90.741	LKT__s__Salmonella_enterica
vfdb---csgA---NP_460115	Major_curlin_subunit	88.079	LKT__s__Salmonella_enterica
vfdb---csgB---NP_460114	Minor_curlin_subunit	91.391	LKT__s__Salmonella_enterica
vfdb---sopE2---NP_460811	Guanine_nucleotide_exchange_factor_sopE2	88.333	LKT__s__Salmonella_enterica
vfdb---sseL---NP_461229	Deubiquitinase_SseL	76.266	LKT__s__Salmonella_enterica
vfdb---flgB---YP_001006764	Flagellar_basal_body_rod_protein_FlgB	76.642	LKT__s__Salmonella_enterica
vfdb---flgC---YP_001006763	Flagellar_basal-body_rod_protein_FlgC	82.09	LKT__s__Salmonella_enterica
vfdb---mgtB---NP_462662	Magnesium-transporting_ATPase_2C_P-type_1	97.137	LKT__s__Salmonella_bongori
vfdb---mgtC---NP_462663	Protein_MgtC	99.559	LKT__s__Salmonella_bongori
vfdb---gmd---YP_001007257	GDP-mannose_4_2C6-dehydratase	79.245	LKT__s__Salmonella_enterica
vfdb---entE---NP_752612	Enterobactin_synthase_component_E	85.019	LKT__s__Salmonella_bongori
vfdb---flhD---YP_001006784	Flagellar_transcriptional_regulator_FlhD	75.862	LKT__s__Salmonella_enterica
vfdb---flhC---YP_001006783	Flagellar_transcriptional_regulator_FlhC	82.383	LKT__s__Salmonella_enterica
vfdb---motA---YP_001006782	Motility_protein_A	82.712	LKT__s__Salmonella_enterica

Virulence factors present in VFDB
www.ncbi.nlm.nih.gov/pubmed/15608208

DB_Hit	Function	Percent_ID	LKT
vfdb---spvR---NP_490531	Virulence_genes_transcriptional_activator	97.643	LKT__s_Salmonella_enterica
vfdb---spvB---NP_490529	Mono_ADP-ribosyl_transferase_SpvB	96.471	LKT__s_Salmonella_enterica
vfdb---spvC---NP_490528	MAPK_phosphothreonine_lyase	97.925	LKT__s_Salmonella_enterica
vfdb---ompA---AAF37887	Outer_membrane_protein_A	98.813	LKT__s_Escherichia_coli
vfdb---mf3---NP_269520	DNA-entry_nuclease	100	LKT__s_Streptococcus_pyogenes
vfdb---gmhA/lpcA---NP_439337	Phosphoheptose_isomerase	76.042	LKT__s_Salmonella_enterica
vfdb---spaQ---NP_461810	hypothetical_protein	98.837	LKT__s_Salmonella_bongori
vfdb---spaR---NP_461809	Surface_presentation_of_antigens_protein_SpaR	96.198	LKT__s_Salmonella_bongori
vfdb---spaS---NP_461808	Surface_presentation_of_antigens_protein_SpaS	96.067	LKT__s_Salmonella_bongori
vfdb---sicA---NP_461807	Chaperone_protein_SicA	100	LKT__s_Salmonella_bongori
vfdb---sipB/sspB---NP_461806	Cell_invasion_protein_SipB	94.941	LKT__s_Salmonella_bongori
vfdb---sipC/sspC---NP_461805	Cell_invasion_protein_SipC	91.932	LKT__s_Salmonella_bongori
vfdb---sipD---NP_461804	Cell_invasion_protein_SipD	86.589	LKT__s_Salmonella_bongori
vfdb---sicP---NP_461800	Chaperone_protein_sicP	80.769	LKT__s_Salmonella_bongori
vfdb---prgH---NP_461795	Protein_PrgH	90.816	LKT__s_Salmonella_bongori
vfdb---prgI---NP_461794	Protein_PrgI	87.5	LKT__s_Salmonella_bongori
vfdb---prgJ---NP_461793	hypothetical_protein	98.02	LKT__s_Salmonella_bongori
vfdb---prgK---NP_461792	Lipoprotein_PrgK	97.222	LKT__s_Salmonella_bongori
vfdb---orgA---NP_461791	Oxygen-regulated_invasion_protein_OrgA	90.625	LKT__s_Salmonella_bongori
vfdb---orgB---NP_461790	Oxygen-regulated_invasion_protein_OrgB	95.495	LKT__s_Salmonella_bongori

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---avrA---NP_461786	Effector_protein_YopJ	76.307	LKT__s_Salmonella_bongori
vfdb---chuS---NP_756169	Hemin_transport_protein_HemS	79.24	LKT__s_Salmonella_bongori
vfdb---shuA---YP_405019	Hemin_receptor	84.161	LKT__s_Salmonella_bongori
vfdb---cdtB---NP_456275	Cytolethal_distending_toxin_subunit_B	81.618	LKT__s_Salmonella_bongori
vfdb---sopA---NP_461011	E3_ubiquitin-protein_ligase_SopA	83.376	LKT__s_Salmonella_bongori
vfdb---mig-14---NP_461708	hypothetical_protein	81.879	LKT__s_Salmonella_enterica
vfdb---iroN---NP_753164	Ferric_enterobactin_receptor	83.081	LKT__s_Salmonella_enterica
vfdb---iroC---NP_753167	Multidrug_efflux_ATP-binding_permease_protein	79.722	LKT__s_Salmonella_enterica
vfdb---iroB---NP_753168	Elloramycin_glycosyltransferase_ElmGT	86.413	LKT__s_Salmonella_enterica
vfdb---icl---YP_177728	Isocitrate_lyase_1	79.673	LKT__s_Segniliparus_rotundus
vfdb---xcpT---NP_251791	Type_II_secretion_system_protein_G	87.943	LKT__s_Pseudomonas_stutzeri
vfdb---xcpS---NP_251792	Type_II_secretion_system_protein_F	78.519	LKT__s_Pseudomonas_stutzeri
vfdb---xcpR---NP_251793	Type_II_secretion_system_protein_E	77.593	LKT__s_Pseudomonas_stutzeri
vfdb---mgtC---NP_462663	Protein_MgtC	92.07	LKT__s_Salmonella_enterica
vfdb---mgtB---NP_462662	Magnesium-transporting_ATPase_2C_P-type_1	95.264	LKT__s_Salmonella_enterica
vfdb---flhA---YP_001006770	Flagellar_biosynthesis_protein_FliA	85.217	LKT__s_Salmonella_enterica
vfdb---cheZ---YP_001006773	Protein_phosphatase_CheZ	79.126	LKT__s_Salmonella_enterica
vfdb---cheY---YP_001006774	Chemotaxis_protein_CheY	90.698	LKT__s_Salmonella_enterica
vfdb---cheB---YP_001006775	Chemotaxis_response_regulator_protein-glutamate_methylesterase	84.527	LKT__s_Salmonella_enterica
vfdb---cheW---YP_001006779	Chemotaxis_protein_CheW	85	LKT__s_Salmonella_enterica

Virulence factors present in VFDB
www.ncbi.nlm.nih.gov/pubmed/15608208

DB_Hit	Function	Percent_ID	LKT
vfdb---pilR---NP_253237	Regulatory_protein_AtoC	85.36	LKT_s_Pseudomonas_stutzeri
vfdb---motA---NP_253641	Motility_protein_A	81.56	LKT_s_Pseudomonas_stutzeri
vfdb---waaA---NP_253675	3-deoxy-D-manno-octulosonic_acid_transferase	78.832	LKT_s_Pseudomonas_stutzeri
vfdb---waaP---NP_253696	Lipopolysaccharide_core_heptose_1_kinase_RfaP	79.478	LKT_s_Pseudomonas_stutzeri
vfdb---waaG---NP_253697	Lipopolysaccharide_core_biosynthesis_protein_RfaG	80.593	LKT_s_Pseudomonas_stutzeri
vfdb---waaF---NP_253699	ADP-heptose--LPS_heptosyltransferase_2	81.05	LKT_s_Pseudomonas_stutzeri
vfdb---grab---NP_269464	Immunoglobulin_G-binding_protein_G	100	LKT_s_Streptococcus_pyogenes
vfdb---lpxC---NP_439302	UDP-3-O-acyl-N-acetylglucosamine_deacetylase	77.303	LKT_s_Escherichia_coli
vfdb---invH---NP_461821	hypothetical_protein	82.313	LKT_s_Salmonella_enterica
vfdb---invF---NP_461820	Invasion_protein_InvF	93.981	LKT_s_Salmonella_enterica
vfdb---invG---NP_461819	Protein_InvG	96.625	LKT_s_Salmonella_enterica
vfdb---invE---NP_461818	Protein_MxiC	99.194	LKT_s_Salmonella_enterica
vfdb---invA---NP_461817	Invasion_protein_InvA	98.978	LKT_s_Salmonella_enterica
vfdb---invB---NP_461816	Surface_presentation_of_antigens_protein_SpaK	97.778	LKT_s_Salmonella_enterica
vfdb---invC---NP_461815	putative_ATP_synthase_SpaL	97.448	LKT_s_Salmonella_enterica
vfdb---invI---NP_461814	hypothetical_protein	90.476	LKT_s_Salmonella_enterica
vfdb---invJ---NP_461813	hypothetical_protein	88.393	LKT_s_Salmonella_enterica
vfdb---spaO---NP_461812	Surface_presentation_of_antigens_protein_SpaO	91.089	LKT_s_Salmonella_enterica
vfdb---spaP---NP_461811	Surface_presentation_of_antigens_protein_SpaP	99.107	LKT_s_Salmonella_enterica
vfdb---spaQ---NP_461810	hypothetical_protein	100	LKT_s_Salmonella_enterica

Virulence factors present in VFDB
www.ncbi.nlm.nih.gov/pubmed/15608208

DB_Hit	Function	Percent_ID	LKT
vfdb---spaR---NP_461809	Surface_presentation_of_antigens_protein_SpaR	96.578	LKT_s_Salmonella_enterica
vfdb---spaS---NP_461808	Surface_presentation_of_antigens_protein_SpaS	96.91	LKT_s_Salmonella_enterica
vfdb---sicA---NP_461807	Chaperone_protein_SicA	99.394	LKT_s_Salmonella_enterica
vfdb---sipB/sspB---NP_461806	Cell_invasion_protein_SipB	92.088	LKT_s_Salmonella_enterica
vfdb---sipC/sspC---NP_461805	Cell_invasion_protein_SipC	91.443	LKT_s_Salmonella_enterica
vfdb---sipD---NP_461804	Cell_invasion_protein_SipD	81.05	LKT_s_Salmonella_enterica
vfdb---sipA/sspA---NP_461803	Cell_invasion_protein_sipA	78.655	LKT_s_Salmonella_enterica
vfdb---sicP---NP_461800	Chaperone_protein_sicP	83.846	LKT_s_Salmonella_enterica
vfdb---prgH---NP_461795	Protein_PrgH	95.028	LKT_s_Salmonella_enterica
vfdb---prgI---NP_461794	Protein_PrgI	92.105	LKT_s_Salmonella_enterica
vfdb---prgJ---NP_461793	hypothetical_protein	97.03	LKT_s_Salmonella_enterica
vfdb---prgK---NP_461792	Lipoprotein_PrgK	98.413	LKT_s_Salmonella_enterica
vfdb---orgA---NP_461791	Oxygen-regulated_invasion_protein_OrgA	90.104	LKT_s_Salmonella_enterica
vfdb---orgB---NP_461790	Oxygen-regulated_invasion_protein_OrgB	97.297	LKT_s_Salmonella_enterica
vfdb---orgC---NP_461789	hypothetical_protein	76.974	LKT_s_Salmonella_enterica
vfdb---rfaD---NP_439271	ADP-L-glycero-D-manno-heptose-6-epimerase	78.247	LKT_s_Escherichia_coli
vfdb---gmhA/lpcA---NP_439337	Phosphoheptose_isomerase	76.042	LKT_s_Salmonella_bongori
vfdb---hyIP---NP_268936	hypothetical_protein	100	LKT_s_Streptococcus_pyogenes
vfdb---kdsA---NP_439706	2-dehydro-3-deoxyphosphoconate_aldolase	81.56	LKT_s_Salmonella_bongori
vfdb---rfaD---NP_439271	ADP-L-glycero-D-manno-heptose-6-epimerase	77.597	LKT_s_Salmonella_bongori

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---flgB---YP_001006764	Flagellar_basal_body_rod_protein_FlgB	76.642	LKT__s__Salmonella_bongori
vfdb---flgC---YP_001006763	Flagellar_basal-body_rod_protein_FlgC	81.343	LKT__s__Salmonella_bongori
vfdb---hasA---NP_270107	Poly-beta-1_2C6-N-acetyl-D-glucosamine_synthase	99.523	LKT__s__Streptococcus_pyogenes
vfdb---hasB---NP_270108	UDP-glucose_6-dehydrogenase	100	LKT__s__Streptococcus_pyogenes
vfdb---hasC---NP_270109	UTP--glucose-1-phosphate-uridylyltransferase	100	LKT__s__Streptococcus_pyogenes
vfdb---icl---YP_177728	Isocitrate_lyase	79.814	LKT__s__Corynebacterium_glutamicum
vfdb---cheW---YP_001006779	Chemotaxis_protein_CheW	85	LKT__s__Salmonella_bongori
vfdb---cheB---YP_001006775	Chemotaxis_response_regulator_protein-glutamate_methylesterase	85.387	LKT__s__Salmonella_bongori
vfdb---cheY---YP_001006774	Chemotaxis_protein_CheY	90.698	LKT__s__Salmonella_bongori
vfdb---cheZ---YP_001006773	Protein_phosphatase_CheZ	79.126	LKT__s__Salmonella_bongori
vfdb---flhA---YP_001006770	Flagellar_biosynthesis_protein_FlhA	85.652	LKT__s__Salmonella_bongori
vfdb---cdtB---NP_456275	Cytolethal_distending_toxin_subunit_B	92.565	LKT__s__Salmonella_enterica
vfdb---fepA---NP_752600	Ferrienterobactin_receptor	82.384	LKT__s__Salmonella_enterica
vfdb---entF---NP_752604	Enterobactin_synthase_component_F	77.975	LKT__s__Salmonella_enterica
vfdb---fepC---NP_752606	Ferric_enterobactin_transport_ATP-binding_protein_FepC	92.015	LKT__s__Salmonella_enterica
vfdb---fepG---NP_752607	Ferric_enterobactin_transport_system_permease_protein_FepG	86.97	LKT__s__Salmonella_enterica
vfdb---fepD---NP_752608	Ferric_enterobactin_transport_system_permease_protein_FepD	88.288	LKT__s__Salmonella_enterica
vfdb---entS---NP_752609	Enterobactin_exporter_EntS	90.465	LKT__s__Salmonella_enterica
vfdb---fepB---NP_752610	Ferrienterobactin-binding_periplasmic_protein	78.616	LKT__s__Salmonella_enterica
vfdb---entC---NP_752611	Isochorismate_synthase_EntC	84.399	LKT__s__Salmonella_enterica

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---entE---NP_752612	Enterobactin_synthase_component_E	86.33	LKT__s__Salmonella_enterica
vfdb---entB---NP_752613	Enterobactin_synthase_component_B	87.018	LKT__s__Salmonella_enterica
vfdb---entA---NP_752614	2_2C3-dihydro-2_2C3-dihydroxybenzoate_dehydrogenase	86.694	LKT__s__Salmonella_enterica
vfdb---gmd---YP_001007257	GDP-mannose_4_2C6-dehydratase	78.763	LKT__s__Pseudomonas_stutzeri
vfdb---fleQ---NP_249788	Regulatory_protein_AtoC	84.167	LKT__s__Pseudomonas_stutzeri
vfdb---motC---NP_250151	Chemotaxis_protein_PomA	80.894	LKT__s__Pseudomonas_stutzeri
vfdb---fliA---NP_250146	RNA_polymerase_sigma_factor_FliA	80.162	LKT__s__Pseudomonas_stutzeri
vfdb---fleN---NP_250145	Flagellum_site-determining_protein_YlxH	86.029	LKT__s__Pseudomonas_stutzeri
vfdb---flhA---NP_250143	Flagellar_biosynthesis_protein_FlhA	87.27	LKT__s__Pseudomonas_stutzeri
vfdb---fliQ---NP_250138	hypothetical_protein	86.517	LKT__s__Pseudomonas_stutzeri
vfdb---fliP---NP_250137	Flagellar_biosynthetic_protein_FliP	86.842	LKT__s__Pseudomonas_stutzeri
vfdb---fliN---NP_250135	Flagellar_motor_switch_protein_FliN	80.503	LKT__s__Pseudomonas_stutzeri
vfdb---fliM---NP_250134	Flagellar_motor_switch_protein_FliM	91.331	LKT__s__Pseudomonas_stutzeri
vfdb---fliI---NP_249795	Flagellum-specific_ATP_synthase	86.696	LKT__s__Pseudomonas_stutzeri
vfdb---fliG---NP_249793	Flagellar_motor_switch_protein_FliG	87.278	LKT__s__Pseudomonas_stutzeri
vfdb---fliF---NP_249792	Flagellar_M-ring_protein	77.243	LKT__s__Pseudomonas_stutzeri
vfdb---fliE---NP_249791	Flagellar_hook-basal_body_complex_protein_FliE	78.899	LKT__s__Pseudomonas_stutzeri
vfdb---flgH---YP_001006758	Flagellar_L-ring_protein	81.081	LKT__s__Salmonella_bongori
vfdb---asIA---AAG10151	Arylsulfatase	96.112	LKT__s__Escherichia_coli
vfdb---gspM---YP_404609	Type_II_secretion_system_protein_M	96.429	LKT__s__Escherichia_coli

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---gspL---YP_404608	Type_II_secretion_system_protein_L	96.503	LKT__s__Escherichia_coli
vfdb---gspC---YP_404599	Type_II_secretion_system_protein_C	92.647	LKT__s__Escherichia_coli
vfdb---fimE---NP_757240	Tyrosine_recombinase_XerD	99.495	LKT__s__Escherichia_coli
vfdb---fimB---NP_757239	Tyrosine_recombinase_XerC	99.5	LKT__s__Escherichia_coli
vfdb---cheB---YP_001006775	Chemotaxis_response_regulator_protein-glutamate_methyltransferase	85.673	LKT__s__Escherichia_coli
vfdb---cheY---YP_001006774	Chemotaxis_protein_CheY	91.473	LKT__s__Escherichia_coli
vfdb---cheZ---YP_001006773	Protein_phosphatase_CheZ	77.67	LKT__s__Escherichia_coli
vfdb---flhA---YP_001006770	Flagellar_biosynthesis_protein_FlhA	85.217	LKT__s__Escherichia_coli
vfdb---htpB---YP_094724	60_kDa_chaperonin	75.665	LKT__s__Salmonella_enterica
vfdb---nanI---NP_561641	Sialidase_A	99.28	LKT__s__Clostridium_perfringens
vfdb---cloSI---NP_561762	Clostripain	99.042	LKT__s__Clostridium_perfringens
vfdb---nagI---NP_561797	O-GlcNAcase_NagJ	98.921	LKT__s__Clostridium_perfringens
vfdb---nanH---YP_695432	Sialidase	100	LKT__s__Clostridium_perfringens
vfdb---kdsA---NP_439706	2-dehydro-3-deoxyphosphooxtonate_aldolase	81.206	LKT__s__Salmonella_enterica
vfdb---fepA---NP_752600	Ferrienterobactin_receptor	81.201	LKT__s__Salmonella_bongori
vfdb---fepC---NP_752606	Ferric_enterobactin_transport_ATP-binding_protein_FepC	99.259	LKT__s__Escherichia_coli
vfdb---fepG---NP_752607	Ferric_enterobactin_transport_system_permease_protein_FepG	97.576	LKT__s__Escherichia_coli
vfdb---fepD---NP_752608	Ferric_enterobactin_transport_system_permease_protein_FepD	99.401	LKT__s__Escherichia_coli
vfdb---entS---NP_752609	Enterobactin_exporter_EntS	99.279	LKT__s__Escherichia_coli
vfdb---fepB---NP_752610	Ferrienterobactin-binding_periplasmic_protein	99.686	LKT__s__Escherichia_coli

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---entC---NP_752611	Isochorismate_synthase_EntC	99.488	LKT__s__Escherichia_coli
vfdb---entE---NP_752612	Enterobactin_synthase_component_E	99.067	LKT__s__Escherichia_coli
vfdb---entB---NP_752613	Enterobactin_synthase_component_B	99.649	LKT__s__Escherichia_coli
vfdb---entA---NP_752614	2_2C3-dihydro-2_2C3-dihydroxybenzoate_dehydrogenase	98.387	LKT__s__Escherichia_coli
vfdb---sopD---NP_461866	Secreted_effector_protein_SopD	82.334	LKT__s__Salmonella_enterica
vfdb---fliQ---YP_001006752	hypothetical_protein	77.528	LKT__s__Escherichia_coli
vfdb---fliP---YP_001006751	Flagellar_biosynthetic_protein_FliP	84.649	LKT__s__Escherichia_coli
vfdb---fliN---YP_001006749	Flagellar_motor_switch_protein_FliN	76.259	LKT__s__Escherichia_coli
vfdb---fliM---YP_001006748	Flagellar_motor_switch_protein_FliM	84.384	LKT__s__Escherichia_coli
vfdb---fliI---YP_001006744	Flagellum-specific_ATP_synthase	83.973	LKT__s__Escherichia_coli
vfdb---fliG---YP_001006742	Flagellar_motor_switch_protein_FliG	83.587	LKT__s__Escherichia_coli
vfdb---fliA---YP_001006726	RNA_polymerase_sigma_factor_FliA	83.193	LKT__s__Escherichia_coli
vfdb---fliC---YP_001006783	Flagellar_transcriptional_regulator_FliC	82.902	LKT__s__Escherichia_coli
vfdb---motA---YP_001006782	Motility_protein_A	81.017	LKT__s__Escherichia_coli
vfdb---cheW---YP_001006779	Chemotaxis_protein_CheW	85.093	LKT__s__Escherichia_coli
vfdb---htpB---YP_094724	60_kDa_chaperonin	75.665	LKT__s__Escherichia_coli
vfdb---espX4---NP_290672	E3_ubiquitin-protein_ligase_SopA	88.662	LKT__s__Escherichia_coli
vfdb---espX5---NP_290699	hypothetical_protein	96.047	LKT__s__Escherichia_coli
vfdb---algW---NP_253136	Periplasmic_pH-dependent_serine_endoprotease_DegQ	75.066	LKT__s__Pseudomonas_stutzeri
vfdb---pilB---NP_253216	Type_II_secretion_system_protein_E	79.365	LKT__s__Pseudomonas_stutzeri

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---pilC---NP_253217	Type_II_secretion_system_protein_F	76.882	LKT_s_Pseudomonas_stutzeri
vfdb---xcpA/pilD---NP_253218	Type_4_prepilin-like_proteins_leader_peptide-processing_enzyme	77.509	LKT_s_Pseudomonas_stutzeri
vfdb---algA---NP_252241	Alginate_biosynthesis_protein_AlgA	79.704	LKT_s_Pseudomonas_stutzeri
vfdb---algU---NP_249453	ECF_RNA_polymerase_sigma-E_factor	91.71	LKT_s_Pseudomonas_stutzeri
vfdb---fepD---NP_752608	Ferric_enterobactin_transport_system_permease_protein_FepD	88.323	LKT_s_Salmonella_bongori
vfdb---fepG---NP_752607	Ferric_enterobactin_transport_system_permease_protein_FepG	88.182	LKT_s_Salmonella_bongori
vfdb---fepC---NP_752606	Ferric_enterobactin_transport_ATP-binding_protein_FepC	92.395	LKT_s_Salmonella_bongori
vfdb---entF---NP_752604	Enterobactin_synthase_component_F	77.821	LKT_s_Salmonella_bongori
vfdb---sinH---NP_461452	Intimin	89.041	LKT_s_Salmonella_bongori
vfdb---gmd---YP_001007257	GDP-mannose_4_2C6-dehydratase	83.152	LKT_s_Coralimargarita_akajimensis
vfdb---gtrB---NP_706258	Prophage_bactoprenol_glucosyl_transferase	89.869	LKT_s_Escherichia_coli
vfdb---gtrA---NP_706257	Prophage_bactoprenol-linked_glucose_translocase	87.5	LKT_s_Escherichia_coli
vfdb---kdsA---NP_439706	2-dehydro-3-deoxyphosphooctonate_aldolase	81.625	LKT_s_Escherichia_coli
vfdb---iucA---NP_755502	N_2-citryl-N_6-acetyl-N_6-hydroxylysine_synthase	88.235	LKT_s_Salmonella_enterica
vfdb---iucB---NP_709455	N_6-hydroxylysine_O-acetyltransferase	87.937	LKT_s_Salmonella_enterica
vfdb---iucC---NP_755500	Aerobactin_synthase	90.972	LKT_s_Salmonella_enterica
vfdb---iucD---NP_709457	L-lysine_N6-monoxygenase	81.941	LKT_s_Salmonella_enterica
vfdb---iutA---NP_755498	Ferric_aerobactin_receptor	88.798	LKT_s_Salmonella_enterica
vfdb---ska---NP_269944	Streptokinase_C	100	LKT_s_Streptococcus_pyogenes
vfdb---smeZ---NP_269959	Exotoxin_type_C	100	LKT_s_Streptococcus_pyogenes

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---lmb---NP_688239	High-affinity_zinc_uptake_system_binding-protein_ZnuA	98.693	LKT__s__Streptococcus_pyogenes
vfdb---fbaA---NP_269969	IgA_FC_receptor	100	LKT__s__Streptococcus_pyogenes
vfdb---scpA---NP_269970	C5a_peptidase	99.915	LKT__s__Streptococcus_pyogenes
vfdb---sic---NP_269972	hypothetical_protein	100	LKT__s__Streptococcus_pyogenes
vfdb---emm---NP_269973	M_protein_2C_serotype_6	100	LKT__s__Streptococcus_pyogenes
vfdb---speB---NP_269985	Streptopain	100	LKT__s__Streptococcus_pyogenes
vfdb---mf/spd---NP_269989	hypothetical_protein	100	LKT__s__Streptococcus_pyogenes
vfdb---hasC---NP_270109	UTP--glucose-1-phosphate_uridylyltransferase	90.604	LKT__s__Streptococcus_pyogenes
vfdb---flgH---YP_001006758	Flagellar_L-ring_protein	80.631	LKT__s__Salmonella_enterica
vfdb---flgI---YP_001006757	Flagellar_P-ring_protein	78.771	LKT__s__Salmonella_enterica
vfdb---plc---NP_560952	Phospholipase_C	99.162	LKT__s__Clostridium_perfringens
vfdb---fepB---NP_752610	Ferrienterobactin-binding_periplasmic_protein	80.818	LKT__s__Salmonella_bongori
vfdb---entC---NP_752611	Isochorismate_synthase_EntC	84.91	LKT__s__Salmonella_bongori
vfdb---lpfA---NP_462541	putative_major_fimbrial_subunit_LpfA	97.701	LKT__s__Salmonella_bongori
vfdb---lpfB---NP_462540	putative_fimbrial_chaperone_LpfB	98.707	LKT__s__Salmonella_bongori
vfdb---lpfC---NP_462539	putative_outer_membrane usher_protein_LpfC	97.15	LKT__s__Salmonella_bongori
vfdb---lpfE---NP_462537	putative_fimbrial_subunit_LpfE	90.857	LKT__s__Salmonella_bongori
vfdb---espL4---NP_290644	hypothetical_protein	96.841	LKT__s__Escherichia_coli
vfdb---nanJ---NP_561469	Sialidase_A	98.721	LKT__s__Clostridium_perfringens
vfdb---flgC---NP_249769	Flagellar_basal-body_rod_protein_FlgC	83.673	LKT__s__Pseudomonas_stutzeri

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---flgD---NP_249770	Basal-body_rod_modification_protein_FlgD	76.382	LKT__s__Pseudomonas_stutzeri
vfdb---flgF---NP_249772	Flagellar_basal-body_rod_protein_FlgF	77.6	LKT__s__Pseudomonas_stutzeri
vfdb---flgG---NP_249773	Flagellar_basal-body_rod_protein_FlgG	91.571	LKT__s__Pseudomonas_stutzeri
vfdb---flgH---NP_249774	Flagellar_L-ring_protein	77.056	LKT__s__Pseudomonas_stutzeri
vfdb---flgI---NP_249775	Flagellar_P-ring_protein	85.014	LKT__s__Pseudomonas_stutzeri
vfdb---mucP---NP_252339	Regulator_of_sigma-E_protease_RseP	77.111	LKT__s__Pseudomonas_stutzeri
vfdb---invI---NP_461814	hypothetical_protein	93.197	LKT__s__Salmonella_bongori
vfdb---invJ---NP_461813	hypothetical_protein	77.083	LKT__s__Salmonella_bongori
vfdb---spaO---NP_461812	Surface_presentation_of_antigens_protein_SpaO	90.099	LKT__s__Salmonella_bongori
vfdb---spaP---NP_461811	Surface_presentation_of_antigens_protein_SpaP	98.214	LKT__s__Salmonella_bongori
vfdb---flgC---YP_001006763	Flagellar_basal-body_rod_protein_FlgC	83.582	LKT__s__Escherichia_coli
vfdb---flgH---YP_001006758	Flagellar_L-ring_protein	81.193	LKT__s__Escherichia_coli
vfdb---flgI---YP_001006757	Flagellar_P-ring_protein	79.05	LKT__s__Escherichia_coli
vfdb---clpC---NP_463763	Negative_regulator_of_genetic_competence_ClpC_MecB	76.398	LKT__s__Thermobacillus_composti
vfdb---entA---NP_752614	2_2C3-dihydro-2_2C3-dihydroxybenzoate_dehydrogenase	89.113	LKT__s__Salmonella_bongori
vfdb---invB---NP_461816	Surface_presentation_of_antigens_protein_SpaK	93.333	LKT__s__Salmonella_bongori
vfdb---invA---NP_461817	Invasion_protein_InvA	97.81	LKT__s__Salmonella_bongori
vfdb---invE---NP_461818	Protein_MxiC	97.832	LKT__s__Salmonella_bongori
vfdb---invG---NP_461819	Protein_InvG	95.027	LKT__s__Salmonella_bongori
vfdb---invF---NP_461820	Invasion_protein_InvF	91.204	LKT__s__Salmonella_bongori

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---invH---NP_461821	hypothetical_protein	82.313	LKT__s_Salmonella_bongori
vfdb---motA---YP_001006782	Motility_protein_A	82.712	LKT__s_Salmonella_bongori
vfdb---flhC---YP_001006783	Flagellar_transcriptional_regulator_FlhC	82.383	LKT__s_Salmonella_bongori
vfdb---ideS/mac---NP_269065	IgM_protease	100	LKT__s_Streptococcus_pyogenes
vfdb---mf2---NP_268944	DNA-entry_nuclease	100	LKT__s_Streptococcus_pyogenes
vfdb---spec---NP_268943	Exotoxin_type_C	100	LKT__s_Streptococcus_pyogenes
vfdb---ykgK/ecpR---NP_286011	HTH-type_transcriptional_regulator_EcpR	95.918	LKT__s_Escherichia_coli
vfdb---yagZ/ecpA---NP_286010	Common_pilus_major_fimbrillin_subunit_EcpA	100	LKT__s_Escherichia_coli
vfdb---yagY/ecpB---NP_286009	putative_fimbrial_chaperone_EcpB	98.649	LKT__s_Escherichia_coli
vfdb---yagX/ecpC---NP_286008	putative_outer_membrane_usher_protein_EcpC	99.524	LKT__s_Escherichia_coli
vfdb---yagW/ecpD---NP_286007	Fimbria_adhesin_EcpD	99.086	LKT__s_Escherichia_coli
vfdb---yagV/ecpE---NP_286006	putative_fimbrial_chaperone_EcpE	97.458	LKT__s_Escherichia_coli
vfdb---sopB/sigD---NP_460064	Inositol_phosphate_phosphatase_SopB	77.897	LKT__s_Salmonella_bongori
vfdb---gmd---YP_001007257	GDP-mannose_4_2C6-dehydratase	79.515	LKT__s_Salmonella_bongori
vfdb---fliG---YP_001006742	Flagellar_motor_switch_protein_FliG	83.283	LKT__s_Salmonella_enterica
vfdb---fliI---YP_001006744	Flagellum-specific_ATP_synthase	84.424	LKT__s_Salmonella_enterica
vfdb---fliM---YP_001006748	Flagellar_motor_switch_protein_FliM	84.685	LKT__s_Salmonella_enterica
vfdb---fliN---YP_001006749	Flagellar_motor_switch_protein_FliN	76.812	LKT__s_Salmonella_enterica
vfdb---fliP---YP_001006751	Flagellar_biosynthetic_protein_FliP	85.903	LKT__s_Salmonella_enterica
vfdb---gogB---NP_461519	E3_ubiquitin-protein_ligase_SspH2	91.975	LKT__s_Salmonella_enterica

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---fbp54---NP_269190	putative_protein_YloA	100	LKT_s_Streptococcus_pyogenes
vfdb---speh---NP_269186	Exotoxin_type_H	100	LKT_s_Streptococcus_pyogenes
vfdb---spei---NP_269185	Enterotoxin_type_E	99.556	LKT_s_Streptococcus_pyogenes
vfdb---slo---NP_268546	Streptolysin_O	100	LKT_s_Streptococcus_pyogenes
vfdb---fctB---YP_281475	hypothetical_protein	100	LKT_s_Streptococcus_pyogenes
vfdb---srtC1---YP_281474	hypothetical_protein	100	LKT_s_Streptococcus_pyogenes
vfdb---fctA---YP_281473	Pilin	100	LKT_s_Streptococcus_pyogenes
vfdb---lepA---YP_281472	hypothetical_protein	100	LKT_s_Streptococcus_pyogenes
vfdb---cpa---YP_281471	Pilin	99.868	LKT_s_Streptococcus_pyogenes
vfdb---ssaU---NP_460387	Yop_proteins_translocation_protein_U	91.168	LKT_s_Salmonella_enterica
vfdb---ssaT---NP_460386	Surface_presentation_of_antigens_protein_SpaR	91.506	LKT_s_Salmonella_enterica
vfdb---ssaS---NP_460385	hypothetical_protein	98.864	LKT_s_Salmonella_enterica
vfdb---ssaR---NP_460384	Flagellar_biosynthetic_protein_FliP	98.605	LKT_s_Salmonella_enterica
vfdb---ssaQ---NP_460383	hypothetical_protein	85.404	LKT_s_Salmonella_enterica
vfdb---ssaP---NP_460382	hypothetical_protein	87.097	LKT_s_Salmonella_enterica
vfdb---ssaO---NP_460381	hypothetical_protein	84.8	LKT_s_Salmonella_enterica
vfdb---ssaN---NP_460380	putative_secretion_system_apparatus_ATP_synthase_SsaN	93.303	LKT_s_Salmonella_enterica
vfdb---ssaV---NP_460379	Secretion_system_apparatus_protein_SsaV	95.888	LKT_s_Salmonella_enterica
vfdb---ssaM---NP_460378	hypothetical_protein	91.736	LKT_s_Salmonella_enterica
vfdb---ssaL---NP_460377	hypothetical_protein	90.606	LKT_s_Salmonella_enterica

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---ssaK---NP_460376	hypothetical_protein	85.268	LKT_s_Salmonella_enterica
vfdb---ssaJ---NP_460374	Yop_proteins_translocation_lipoprotein_J	89.157	LKT_s_Salmonella_enterica
vfdb---ssaH---NP_460372	hypothetical_protein	89.333	LKT_s_Salmonella_enterica
vfdb---ssaG---NP_460371	hypothetical_protein	92.958	LKT_s_Salmonella_enterica
vfdb---sseG---NP_460370	hypothetical_protein	83.478	LKT_s_Salmonella_enterica
vfdb---sseF---NP_460369	hypothetical_protein	76.654	LKT_s_Salmonella_enterica
vfdb---sscB---NP_460368	hypothetical_protein	94.326	LKT_s_Salmonella_enterica
vfdb---sseE---NP_460367	hypothetical_protein	86.861	LKT_s_Salmonella_enterica
vfdb---sseC---NP_460365	Secreted_effector_protein_SseC	79.339	LKT_s_Salmonella_enterica
vfdb---sscA---NP_460364	hypothetical_protein	91.72	LKT_s_Salmonella_enterica
vfdb---sseB---NP_460363	Secreted_effector_protein_SseB	78.283	LKT_s_Salmonella_enterica
vfdb---ssaE---NP_460361	hypothetical_protein	89.744	LKT_s_Salmonella_enterica
vfdb---ssaD---NP_460360	hypothetical_protein	89.578	LKT_s_Salmonella_enterica
vfdb---ssaC---NP_460359	Type_III_secretion_system_outer_membrane_protein_SpiA	93.964	LKT_s_Salmonella_enterica
vfdb---spiC/ssaB---NP_460358	Salmonella_pathogenicity_island_2_protein_C	89.764	LKT_s_Salmonella_enterica
vfdb---ureG---NP_206868	Urease_accessory_protein_UreG	79.695	LKT_s_Hungateiclostridium_thermocellum
vfdb---ompA---AAF37887	Outer_membrane_protein_A	92	LKT_s_Salmonella_enterica
vfdb---misL---NP_462656	Outer_membrane_protein_icsA_autotransporter	86.613	LKT_s_Salmonella_bongori
vfdb---pilP---NP_253728	hypothetical_protein	75.949	LKT_s_Pseudomonas_stutzeri
vfdb---pilO---NP_253729	hypothetical_protein	83.092	LKT_s_Pseudomonas_stutzeri

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---pilN---NP_253730	hypothetical_protein	80.952	LKT_s_Pseudomonas_stutzeri
vfdb---pilM---NP_253731	Cell_division_protein_FtsA	87.853	LKT_s_Pseudomonas_stutzeri
vfdb---algR---NP_253948	Sensory_transduction_protein_LytR	86.694	LKT_s_Pseudomonas_stutzeri
vfdb---algZ---NP_253949	Sensor_histidine_kinase_BtsS	78.841	LKT_s_Pseudomonas_stutzeri
vfdb---spg---NP_268582	Exotoxin_type_C	100	LKT_s_Streptococcus_pyogenes
vfdb---aslA---AAG10151	Arylsulfatase	82.289	LKT_s_Salmonella_enterica
vfdb---spej---NP_268735	Exotoxin_type_C	100	LKT_s_Streptococcus_pyogenes
vfdb---psaA---NP_346089	Meta_ABC_transporter_substrate-binding_lipoprotein	76.299	LKT_s_Streptococcus_pyogenes
vfdb---fimH---NP_757248	Type_1_fimbrin_D-mannose_specific_adhesin	98.667	LKT_s_Escherichia_coli
vfdb---fimG---NP_757247	Protein_FimG	97.605	LKT_s_Escherichia_coli
vfdb---fimF---NP_757245	Protein_FimF	98.295	LKT_s_Escherichia_coli
vfdb---fimD---NP_757244	Outer_membrane usher_protein_FimD	99.089	LKT_s_Escherichia_coli
vfdb---fimC---NP_757243	Chaperone_protein_FimC	98.34	LKT_s_Escherichia_coli
vfdb---fimI---NP_757242	putative_major_fimbrial_subunit_LpfA	98.182	LKT_s_Escherichia_coli
vfdb---fimA---NP_757241	Type-1_fimbrial_protein_2C_A_chain	92.308	LKT_s_Escherichia_coli
vfdb---sseJ---NP_460590	Secreted_effector_protein_SseJ	77.586	LKT_s_Salmonella_enterica
vfdb---relA---NP_217099	Bifunctional_p_ppGpp_synthase_hydrolase_RelA	77.793	LKT_s_Segniliparus_rotundus
vfdb---nagJ---NP_562150	O-GlcNAcase_NagJ	99.101	LKT_s_Clostridium_perfringens
vfdb---nagK---NP_562195	Hyaluronoglucosaminidase	97.526	LKT_s_Clostridium_perfringens
vfdb---sopB/sigD---NP_460064	Inositol_phosphate_phosphatase_SopB	90.196	LKT_s_Salmonella_enterica

Virulence factors present in VFDB
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DB_Hit	Function	Percent_ID	LKT
vfdb---fes---NP_752602	Enterochelin_esterase	95.5	LKT_f_Enterobacteriaceae
vfdb---fepA---NP_752600	Ferrienterobactin_receptor	99.196	LKT_f_Enterobacteriaceae
vfdb---entD---NP_752599	Enterobactin_synthase_component_D	95.547	LKT_f_Enterobacteriaceae
vfdb---pilJ---NP_249102	Methyl-accepting_chemotaxis_protein_McpQ	83.284	LKT_s_Pseudomonas_stutzeri
vfdb---pilI---NP_249101	Chemotaxis_protein_CheW	81.921	LKT_s_Pseudomonas_stutzeri
vfdb---pilH---NP_249100	Response_regulator_PleD	92.562	LKT_s_Pseudomonas_stutzeri
vfdb---pilG---NP_249099	Transcriptional_regulatory_protein_WalR	92.593	LKT_s_Pseudomonas_stutzeri
vfdb---pilU---NP_249087	Twitching_mobility_protein	87.696	LKT_s_Pseudomonas_stutzeri
vfdb---pilT---NP_249086	Twitching_mobility_protein	94.186	LKT_s_Pseudomonas_stutzeri
vfdb---algB---NP_254170	Alginate_biosynthesis_transcriptional_regulatory_protein_AlgB	80.178	LKT_s_Pseudomonas_stutzeri
vfdb---gmd---YP_001007257	GDP-mannose_4_2C6-dehydratase	79.301	LKT_s_Hirschia_baltica

Most common FeatType signatures

CDS

Most common Product signatures

Most common Coils signatures

Coil

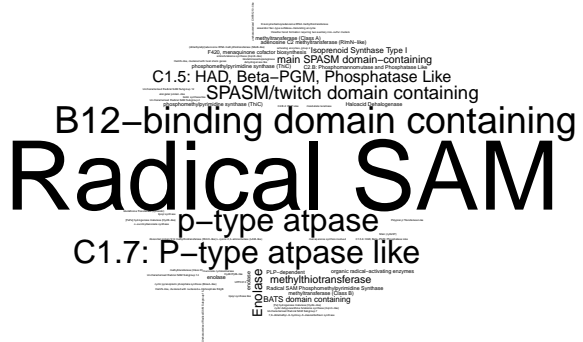
Most common Phobius signatures

Signal peptide region

Most common PIRSF signatures



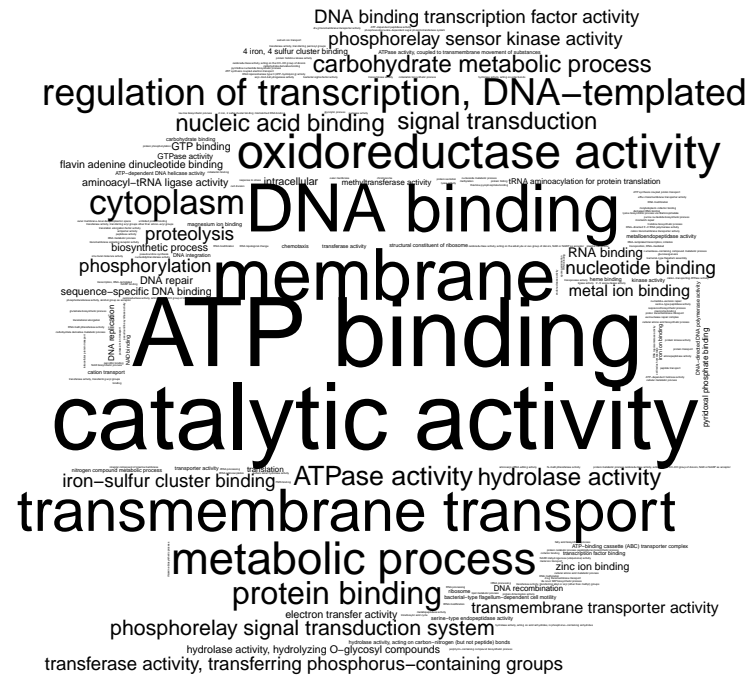
Most common SFLD signatures



Most common SMART signatures

E-Z type HEAT repeats
Phosphopantetheine attachment site

Most common GO signatures



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